

**Figure 1: Full length INSP101 (SEQ ID NO:6) versus P01241, Pituitary growth hormone (GH-N) from *H. sapiens*:**

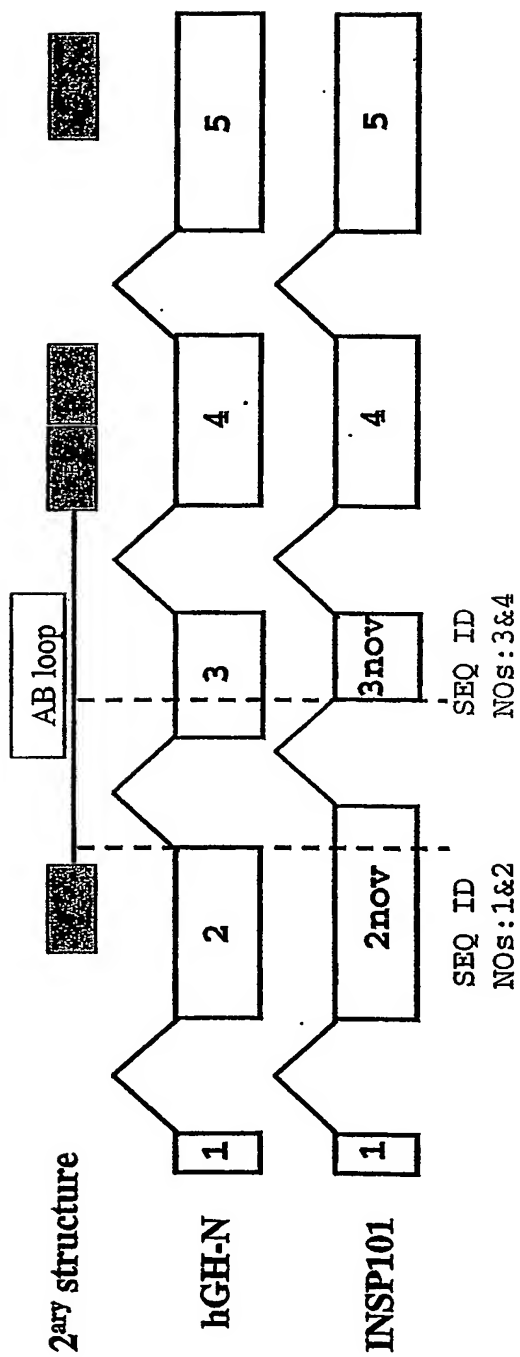
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Query: 1  MATGSRTSLLLAFLGCLLPWLQEGSAFPTIPLSRLFDNAMLRAHRLHQLAFDITYQEFVSS 60
          MATGSRTSLLLAFLGCLLPWLQEGSAFPTIPLSRLFDNAMLRAHRLHQLAFDITYQEF  +
Sbjct: 1  MATGSRTSLLLAFLGCLLPWLQEGSAFPTIPLSRLFDNAMLRAHRLHQLAFDITYQEFEEA 60
                                     ***

Query: 61  W-----GMESIPTPSNREETQQKSNLELLRISLLLIQSWLEPVQFLR 102
          +
          ESIPTPSNREETQQKSNLELLRISLLLIQSWLEPVQFLR
Sbjct: 61  YIPKEQKYSFLQNPQTSLCFSESIPTPSNREETQQKSNLELLRISLLLIQSWLEPVQFLR 120
          *****

Query: 103 SVFANSLVYGASDSNVYDLLKDLEEGIQTLMGRLEDGSPRTGQIFKQTYSKFDTNSHNDD 162
          SVFANSLVYGASDSNVYDLLKDLEEGIQTLMGRLEDGSPRTGQIFKQTYSKFDTNSHNDD
Sbjct: 121 SVFANSLVYGASDSNVYDLLKDLEEGIQTLMGRLEDGSPRTGQIFKQTYSKFDTNSHNDD 180

Query: 163 ALLKNYGLLYCFRKMDKVETFLRIVQCRSVEGSCGF 199
          ALLKNYGLLYCFRKMDKVETFLRIVQCRSVEGSCGF
Sbjct: 181 ALLKNYGLLYCFRKMDKVETFLRIVQCRSVEGSCGF 217
```

Figure 2: Gene Structure



**Figure 3: Predicted nucleotide sequence of INSP101 with translation. Underlined sequence denotes the predicted signal sequence**

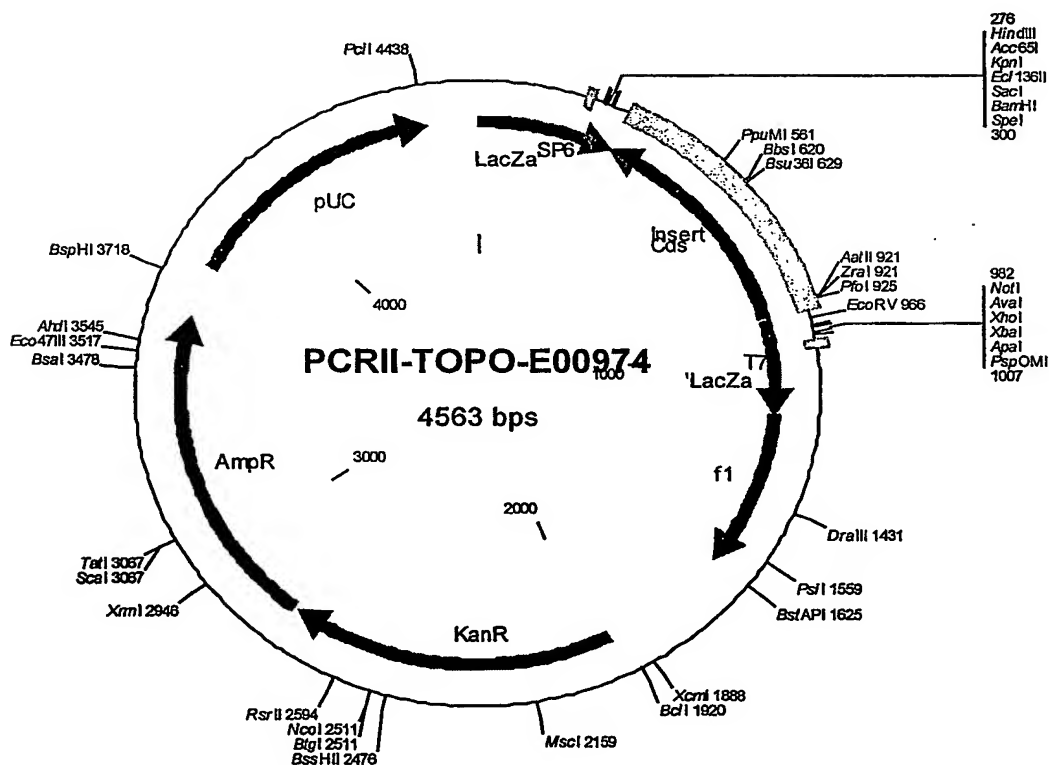
```
1  atggctacag gctcccggaac gtcctgctc ctggcttttg gcctgctctg
   m a t q s r t s l l l a f q l l
51  cctgccctgg cttcaagagg gcagtgcctt cccaaccatt cccttatcca
   c l p w l q e q s a f p t i p l s
101 ggctttttga caacgctatg ctccgcgcc atcgtctgca ccagctggcc
    r l f d n a m l r a h r l h q l a
151 tttgacacct accaggagtt tgtaagctct tggggaatgg agtctattcc
    f d t y q e f v s s w g m e s i
201 gacaccctcc aacagggagg aaacacaaca gaaatccaac ctagagctgc
    p t p s n r e e t q q k s n l e l
251 tccgcatctc cctgctgctc atccagtcgt ggctggagcc cgtgcagttc
    l r i s l l l i q s w l e p v q f
301 ctcaggagtg tcttcgcaa cagcctggtg tacggcgctt ctgacagcaa
    l r s v f a n s l v y g a s d s
351 cgtctatgac ctccataaagg acctagagga aggcattcaa acgctgatgg
    n v y d l l k d l e e g i q t l m
401 ggaggctgga agatggcagc ccccggaactg ggcagatctt caagcagacc
    g r l e d g s p r t g q i f k q t
451 tacagcaagt tcgacacaaa ctacacaaac gatgacgcac tactcaagaa
    y s k f d t n s h n d d a l l k
501 ctacgggctg ctctactgct tcaggaagga catggacaag gtcgagacat
    n y g l l y c f r k d m d k v e t
551 tcctgcgcat cgtgcagtgc cgctctgtgg agggcagctg tggcttc
    f l r i v q c r s v e g s c g f
```

**Figure 4: Map of plasmid pCRII-TOPO-E00974**

Molecule: product2, 4563 bps DNA Circular  
 File Name: 13686[1].cm5

Description: Ligation of inverted NoName into PCRII-TOPO-open

Type	Start	End	Name	Description
GENE	1	336	LacZa'	
REGION	239	256	SP6	Sp6 promoter
GENE	943	338	C Cds	Inserted cds (E00974)
REGION	949	337	C Insert	Inserted PCR product
GENE	950	1201	'LacZa	
REGION	1019	1038	T7	T7 promoter
GENE	1203	1617	f1	f1 ori
GENE	1951	2745	KanR	Kanamycin resistance gene
GENE	2763	3623	AmpR	Ampicillin resistance gene
GENE	3768	4441	pUC	pUC ori



**Figure 5: Alignment of INSP101 with plasmid #13686**

top = INSP101

bottom = 13686

INSPI101-B1P-5'-F

INSPI101  
13686 ATGGCTACAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGCCCTGG  
ATGGCTACAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGCCCTGG

INSPI101  
13686 CTTCAGAGGGCAGTGCCTTCCCAACCATTCCTTATCCAGGCTTTTGGACAACGCTATG  
CTTCAGAGGGCAGTGCCTTCCCAACCATTCCTTATCCAGGCTTTTGGACAACGCTATG

INSPI101  
13686 CTCCGCGCCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTTGT-----A  
CTCCGCGCCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTTAAACCCCCAG

INSPI101  
13686 AGCTCTGGGGAAT---GGAGTCTATTCCGACACCCTCCAACAGGGAGGAAACACAACAG  
ACCTCCCTCTGTTTCTCAGAGTCTATTCCGACACCCTCCAACAGGGAGGAAACACAACAG

INSPI101-3'-F

INSPI101  
13686 AAATCCAACCTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCCAGTCGTGGCTGGAGCCC  
AAATCCAACCTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCCAGTCGTGGCTGGAGCCC

INSPI101  
13686 GTGCAGTTCCTCAGGAGTGTCTTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGCAAC  
GTGCAGTTCCTCAGGAGTGTCTTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGCAAC

INSPI101  
13686 GTCTATGACCTCCTAAAGGACCTAGAGGAAGGCATCCAAACGCTGATGGGGAGGCTGGAA  
GTCTATGACCTCCTAAAGGACCTAGAGGAAGGCATCCAAACGCTGATGGGGAGGCTGGAA

INSPI101  
13686 GATGGCAGCCCCGGACTGGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAAC  
GATGGCAGCCCCGGACTGGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAAC

INSPI101  
13686 TCACACAACGATGACGCACTACTCAAGAACTACGGGCTGCTCTACTGCTTCAGGAAGGAC  
TCACACAACGATGACGCACTACTCAAGAACTACGGGCTGCTCTACTGCTTCAGGAAGGAC

INSPI101  
13686 ATGGACAAGGTCGAGACATTCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGT  
ATGGACAAGGTCGAGACATTCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGT

INSPI101-3'-R

INSPI101  
13686 GGCTTC  
GGCTTC

**Figure 6: Nucleotide sequence and translation of cloned INSP101 product**

1 acaagtttgt acaaaaaagc aggcctcgcc accatggcta caggctcccg  
m a t g s

51 gacgtccctg ctccctggctt ttggcctgct ctgcctgccc tggcttcaag  
r t s l l l a f g l l c l p w l q

101 agggcagtgc cttcccaacc attcccttat ccaggctttt tgacaacgct  
e g s a f p t i p l s r l f d n a

151 atgctccgcg cccatcgtct gcaccagctg gcctttgaca cctaccagga  
m l r a h r l h q l a f d t y q

201 gtttgtaagc tcttggggaa tggagtctat tccgacaccc tccaacaggg  
e f v s s w g m e s i p t p s n r

251 aggaaacaca acagaaatcc aacctagagc tgctccgcat ctccctgctg  
e e t q q k s n l e l l r i s l l

301 ctcattccagt cgtggctgga gcccgctgcag ttcctcagga gtgtcttcgc  
l i q s w l e p v q f l r s v f

351 caacagcctg gtgtacggcg cctctgacag caacgtctat gacctcctaa  
a n s l v y g a s d s n v y d l l

401 aggacctaga ggaaggcatc caaacgctga tggggaggct ggaagatggc  
k d l e e g i q t l m g r l e d g

451 agcccccgga ctgggcagat cttcaagcag acctacagca agttcgacac  
s p r t g q i f k q t y s k f d

501 aaactcacac aacgatgaag cactactcaa gaactacggg ctgctctact  
t n s h n d d a l l k n y g l l y

551 gcttcaggaa ggacatggac aaggctcgaga cattcctgcg catcgtgcag  
c f r k d m d k v e t f l r i v q

601 tgccgctctg tggagggcag ctgtggcttc caccatcacc atcaccattg  
c r s v e g s c g f h h h h h h

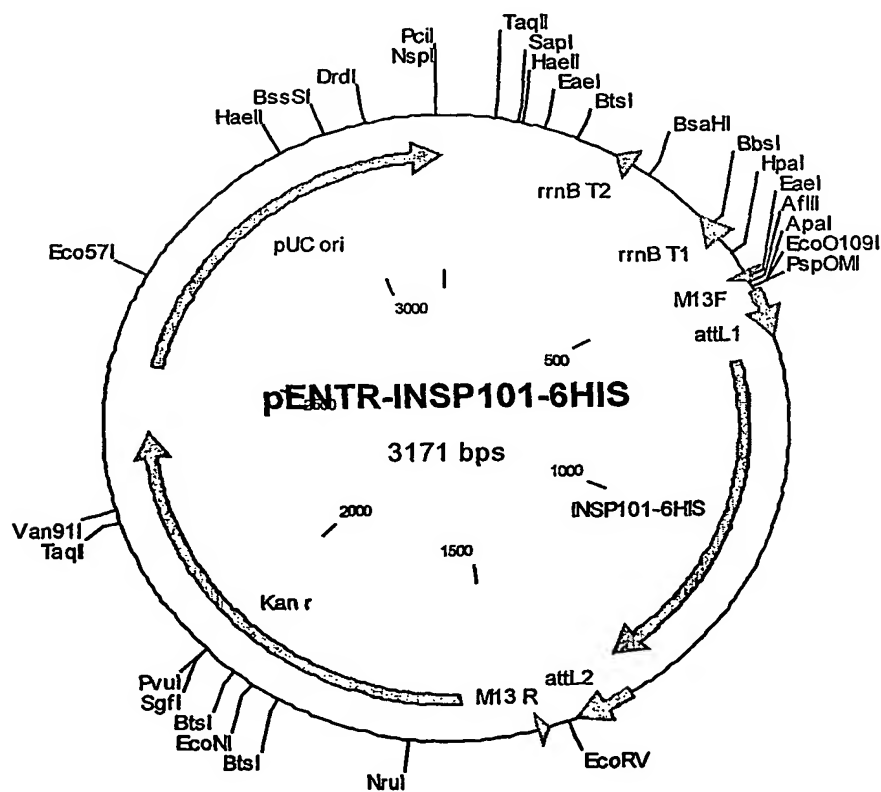
651 aaaccagct ttcttgtaga aagtgg

**Figure 7: Map of pENTR-INSP101-6HIS**

Molecule: pENTR-INSP101-6HIS, 3171 bps DNA Circular  
 File Name: pENTR-INSP101-6HIS-V1.cm5, dated 21 Nov 2003

Description: Ligation of B1b2-orf.seq\* into pDONR221\*

Type	Start	End	Name	Description
REGION	295	268	C rrnB T2	transcription termination sequence
REGION	470	427	C rrnB T1	transcription termination sequence
REGION	537	552	M13F	forward primer
REGION	570	651	attL1	
GENE	677	1291	INSP101-6HIS	
REGION	1306	1394	attL2	
REGION	1452	1436	C M13 R	reverse primer
GENE	1565	2374	Kan r	
GENE	2495	3168	pUC ori	



**Figure 8: Map of pEAK12d-INSP101-6HIS**

Molecule: pEAK12d-INSP101-6HIS-V1, 7564 bps DNA Circular  
 File Name: pEAK12d-INSP101-6HIS-V1.cm5, dated 17 Jul 2003

Description: pEAK12 DES with two recombination sites attR1 and attR2 between which the cDNA is inserted

Type	Start	End	Name	Description
REGION	2	595	pmb-ori	
GENE	596	1519	Amp	
REGION	1690	2795	EF-1alpha	
REGION	2703	2722	peak12-F	forward primer
REGION	2855	2874	attB1	
GENE	2888	3502	INSP101-6HIS	
REGION	3510	3531	attB2	
REGION	3538	3966	'A	poly A/splice
REGION	3652	3633	C peak12-R	reverse primer
GENE	4585	3967	C PUR	PUROMYCIN
REGION	4809	4586	C tK	tK promoter
REGION	5304	4810	C Ori P	
GENE	7356	5304	C EBNA-1	
REGION	7357	7556	sv40	

